REMARKS

Amendments to the Claims

Claims 4 and 43-44 have been amended herein. Support for these amendments can be found at [0011], [0143], [0145], and [0155]. Claims 5 and 12 have been canceled. No new matter has been added by these amendments.

Rejection Under 35 U.S.C. § 112 Second Paragraph

The rejection of claims 4, 43 and 44 under 35 USC 112, first paragraph remain, based on an alleged lack of enablement. According to the Examiner, the skilled artisan would not have reasonably expected a polypeptide having less than 100% identity over the full length of SEQ ID NO:5 to share the same function as the polypeptide of SEQ ID NO:1. Also, according to the Examiner, functional activity is not sufficiently conveyed by these claims because an antibody epitope which may be as small as 6-15 shared amino acid residues would not place any limitations on the function of the protein containing the polypeptide sequence. Therefore, according to the Examiner, the recitation of percent identity language, in the absence of testable function and limitations regarding the sequence length over which the percent identity is required, does not allow the skilled artisan to make and use the encoding nucleic acids. The Examiner suggests amending part (i) of claim 4 to read "the" nucleotide sequence as set forth in SEQ ID NO:5 to provide a limitation to the full sequence of SEQ ID NO:5, and not just any sequence encompassed by SEQ ID NO:5. Finally, according to the Examiner, a polypeptide encoded by "a nucleotide sequence capable of hybridizing to full-length SEQ ID NO: 5" is ambiguous because the translation of the complementary sequence of a nucleic acid sequence of SEQ ID NO:5 would not encode WARP.

Applicants respectfully request this rejection be withdrawn given the claim amendments. As a preliminary matter, Applicants respectfully suggest that a better way of addressing the Examiner's concern that the entire sequence be referenced is to expressly state this in the claims: to precede the first reference to the sequence with the definite article "the"

would lack adequate antecedence. Applicants have amended claims 4, 43 and 44 to refer to the entire nucleotide sequence.

Applicants submit that amended claims 4, 43 and 44 are fully enabled. First, the rejection against claim 4 is rendered moot by its amendment since the claim no longer makes reference to the functional language upon which this rejection was based. Amended claim 43 and dependent claim 44 are directed to an isolated polypeptide, wherein said polypeptide comprises a von Willebrand Factor A-Related Protein (WARP) encoded by a nucleotide sequence selected from the group consisting of:

i. a nucleotide sequence having at least 95% identity to the entire nucleotide sequence set forth in SEQ ID NO:5; and

ii. a nucleotide sequence having at least 99% identity to the entire nucleotide sequence set forth in SEQ ID NO:5, and wherein said polypeptide comprises one von Willebrand Factor A (VA)-like domain, a putative metal ion-dependent adhesion site (MIDAS) motif, two fibronectin type III (F3)-like repeats, and a short proline and arginine-rich segment. Applicants assert that these amendments provide for sufficient functional activity, since one would presume that a polypeptide would be share the same functional activity as that of SEQ ID NO:5, if it was to have at least 95% or 99% identity to the entire nucleotide sequence set forth in SEQ ID NO:5 while also comprising the functional domains recited.

The specification provides that a VA-like domain, MIDAS motif, fibronectin type III-like repeats, and short proline and arginine-rich segments are important WARP structural domains serving important functions in the mouse WARP. When conserved sequences are considered, the mouse the human WARP proteins share 95% identity, therefore, it is presumed that the function of the human WARP protein would share these same functional characteristics. (*See e.g.,* [0142], Figure 1A showing the nucleotide and amino acid sequence of mouse WARP, Figure 1B showing the modular structure of WARP to represent conserved ECM protein modules, Figure 1C showing the alignment of mouse and human WARP amino acid sequences identifying important functional domains, Example 11, and paragraphs [0143] and [0144]).

In identifying human WARP by searching the genomic database with the mouse WARP protein sequence, Applicants have disclosed important homologous WARP domain regions. ([0143]). Both the human and mouse homologs have a VA-domain of approximately 200 amino acids with a putative MIDAS motif. ([0145]). As discussed in the specification, VA domains appear to play an important role in protein-protein interactions. ([0006]). In addition, the MIDAS motif binds divalent cations and gives I domains of integrins their adhesive and ligand binding properties ([0005]). Also, the C-terminus at the end of the second F3 repeat of 21 amino acids in length (24 in the human sequence) is rich in proline and arginine residues, which *did not show homology to any other protein by extensive database searching* (emphasis added), suggesting that this repeat is specific to WARP. ([0143]).

Applicants assert that amended claims 43 and 44 now explicitly provide for conserved functional regions on SEQ ID NO:5. Since the amended claims provide testable functional domains which allow the skilled artisan to make and use the encoding nucleic acids commensurate with the scope of these claims, Applicants respectfully request that this rejection be withdrawn.

Claim 44 is rejected under 35 USC 112, second paragraph, for being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention. The Examiner refers to claim 43, but Applicants assume this was a typographical error, and the claim at issue is claim 44, therefore, Applicants respond accordingly. According to the Examiner claim 44 refers to "99% similar," whereas base claim 43 refers to "99% identity." Applicants have amended claim 44 to read "99% identity," and respectfully request that this rejection be withdrawn.

Rejection Under 35 U.S.C. § 112 First Paragraph

Claims 4 and 43-44 are rejected under 35 USC 112, first paragraph, for containing new matter which was not described in the specification. Applicants respectfully traverse. According to the Examiner, the specification as filed does not provide sufficient support for "said polypeptide specifically binds to an antibody directed toward a von Willebrand Factor type A domain." Further, according to the Examiner, the specification and the claims as originally

filed only contemplate an antibody to specific sequences.

Claims 4 and 43 have been amended to remove language upon which this rejection is based, thus rendering this rejection moot. Amended claim 4 is now directed to an isolated polypeptide, wherein the polypeptide is a von Willebrand Factor A-Related Protein (WARP) comprising the entire amino acid sequence set forth in SEQ ID NO:6, support for which is found at [0155] of the published application. Further, support for amended claims 43 and 44 can be found at [0011], [0143], and [0145]. As such, no new matter has been introduced, Applicants therefore respectfully request that this rejection be withdrawn.

Rejection Under 35 U.S.C. § 102(e)

Claims 4, and 43-44 are rejected under 35 USC 102(e) for being anticipated by U.S. Patent No. 7,368,531 to Rosen et al. ("Rosen"). According to the Examiner, Rosen teaches a 734 bp nucleic acid sequence which has 99.7% similarity to SEQ ID NO:5. Applicants respectfully traverse this rejection in view of the claim amendments. Firstly, this rejection should be withdrawn with respect to claim 4 since it no longer refers to SEQ ID NO:5. In addition, claims 43-44 now refer to a nucleotide sequence having an identity to the entire nucleotide sequence set forth in SEQ ID NO:5. Since the sequence in Rosen is much shorter than the full length sequence of SEQ ID NO:5 (1254 bp), Rosen has not taught each and every element of the claims. Accordingly, Applicants respectfully request that this rejection be withdrawn.

Claims 4 and 43-44 are rejected under 35 USC 102(e) as being anticipated by U.S. Patent No. 7,129,338 to Ota et al. ("Ota"). According to the Examiner, Ota teaches a 550 bp nucleic acid sequence which has 97% similarity to SEQ ID NO:5 thereby reading on claim 43-45. As discussed above, this rejection should be withdrawn with respect to amended claim 4 since it no longer recites SEQ ID NO:5. Further, claims 43-44 now refer a nucleotide sequence having an identity to the entire nucleotide sequence set forth in SEQ ID NO:5. Since the sequence in Ota is much shorter than the full length sequence of SEQ ID NO:5 (1254 bp), Ota

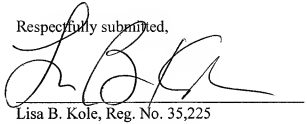
has not taught each and every element of the claims. Accordingly, Applicants respectfully request that this rejection be withdrawn.

Conclusion

Based on the above remarks and amendments, Applicants respectfully request a finding of allowance of claims 4, and 43-44. If the United States Patent and Trademark Office deems that an interview is appropriate, Applicants would appreciate the opportunity for such an interview. The Examiner is invited to contact the undersigned to discuss any outstanding matters that may be resolved by telephone.

Applicants believe that no fees are required. Should fees be required, or if fees are overpaid, the Director is hereby authorized to charge any required fees or credit any overpayments to Deposit Account 02-4377 of Baker Botts, LLP.

Respectfully submitted,



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